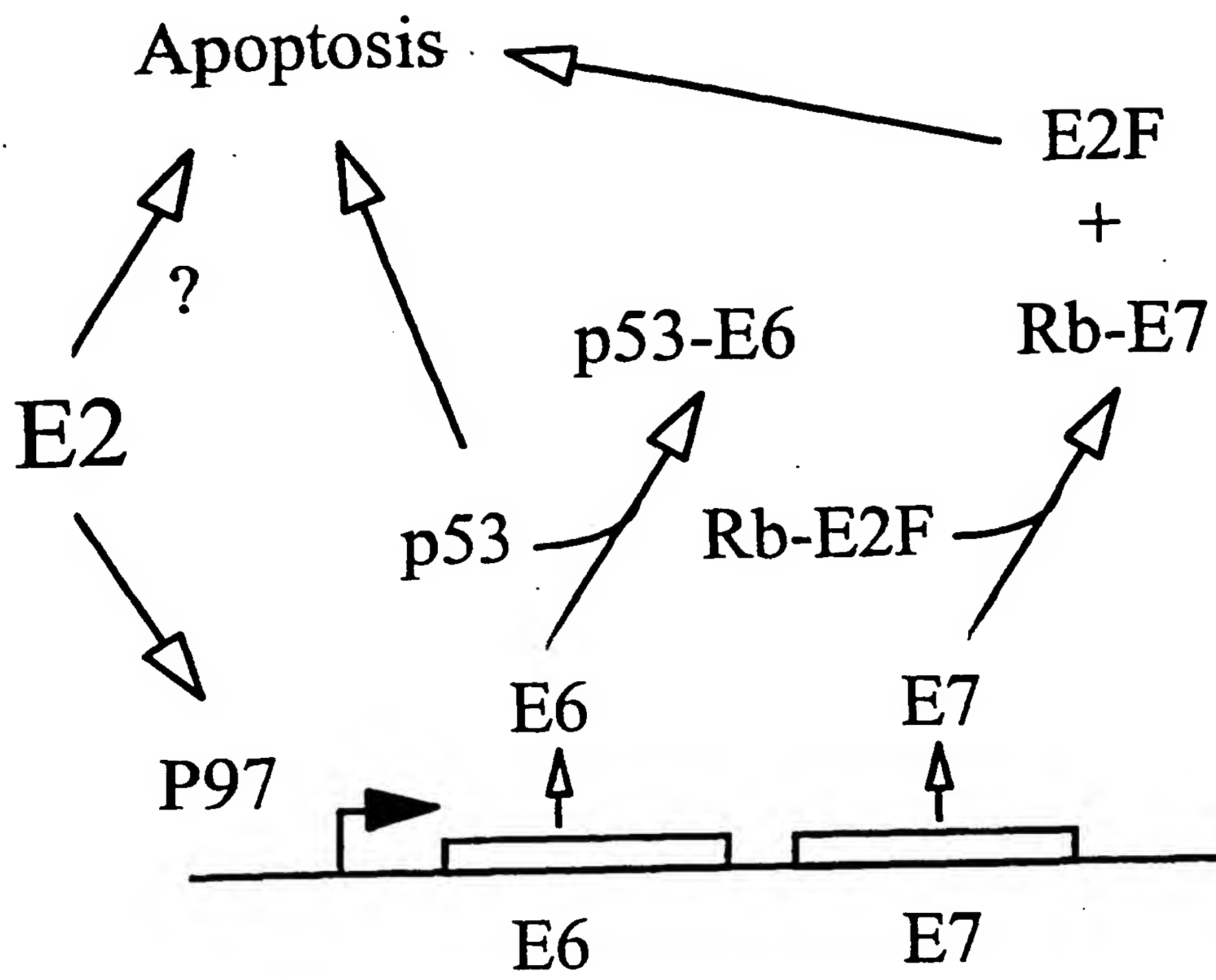


Fig. 1

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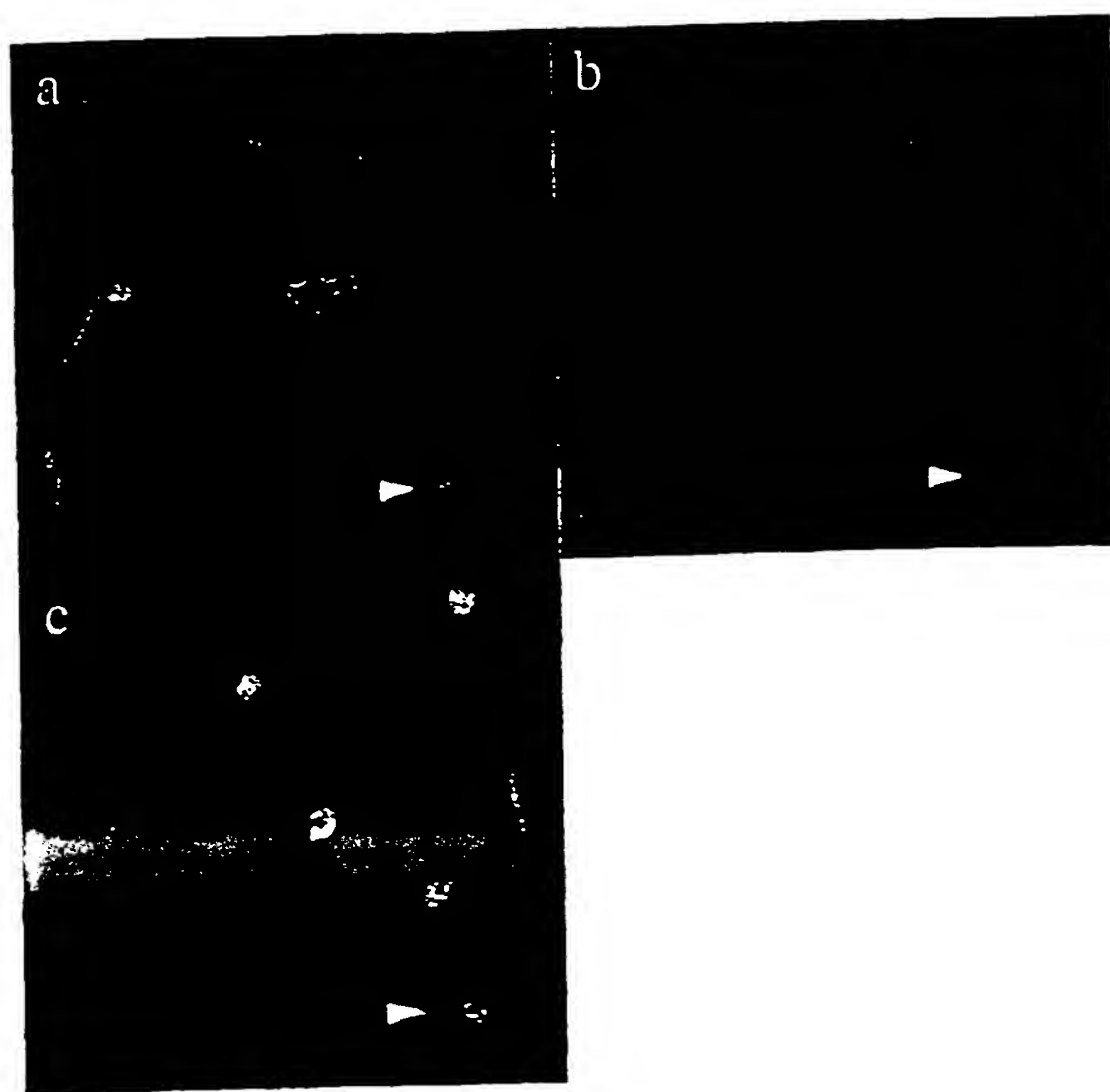
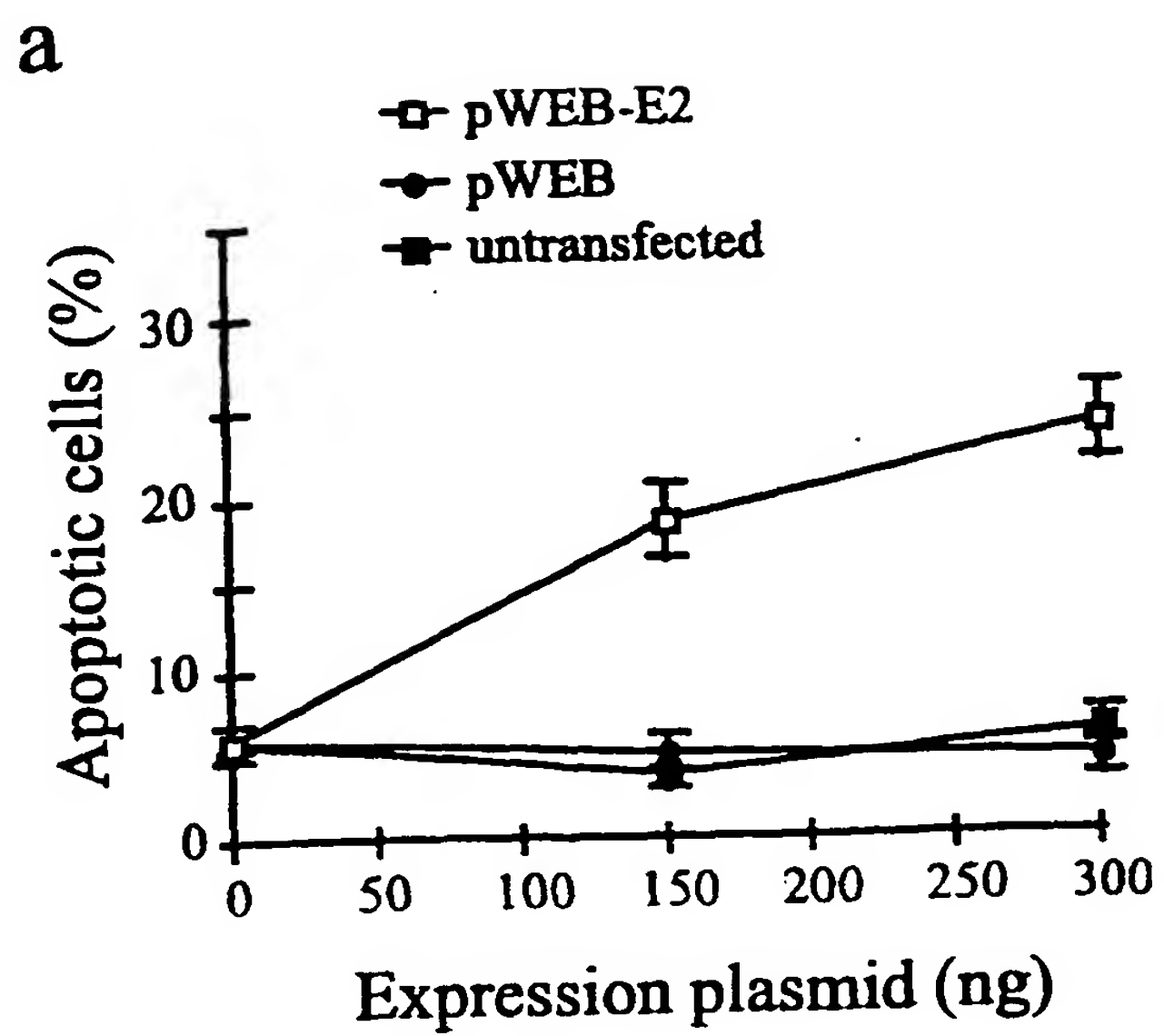


Fig. 2

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Fig. 3A



b

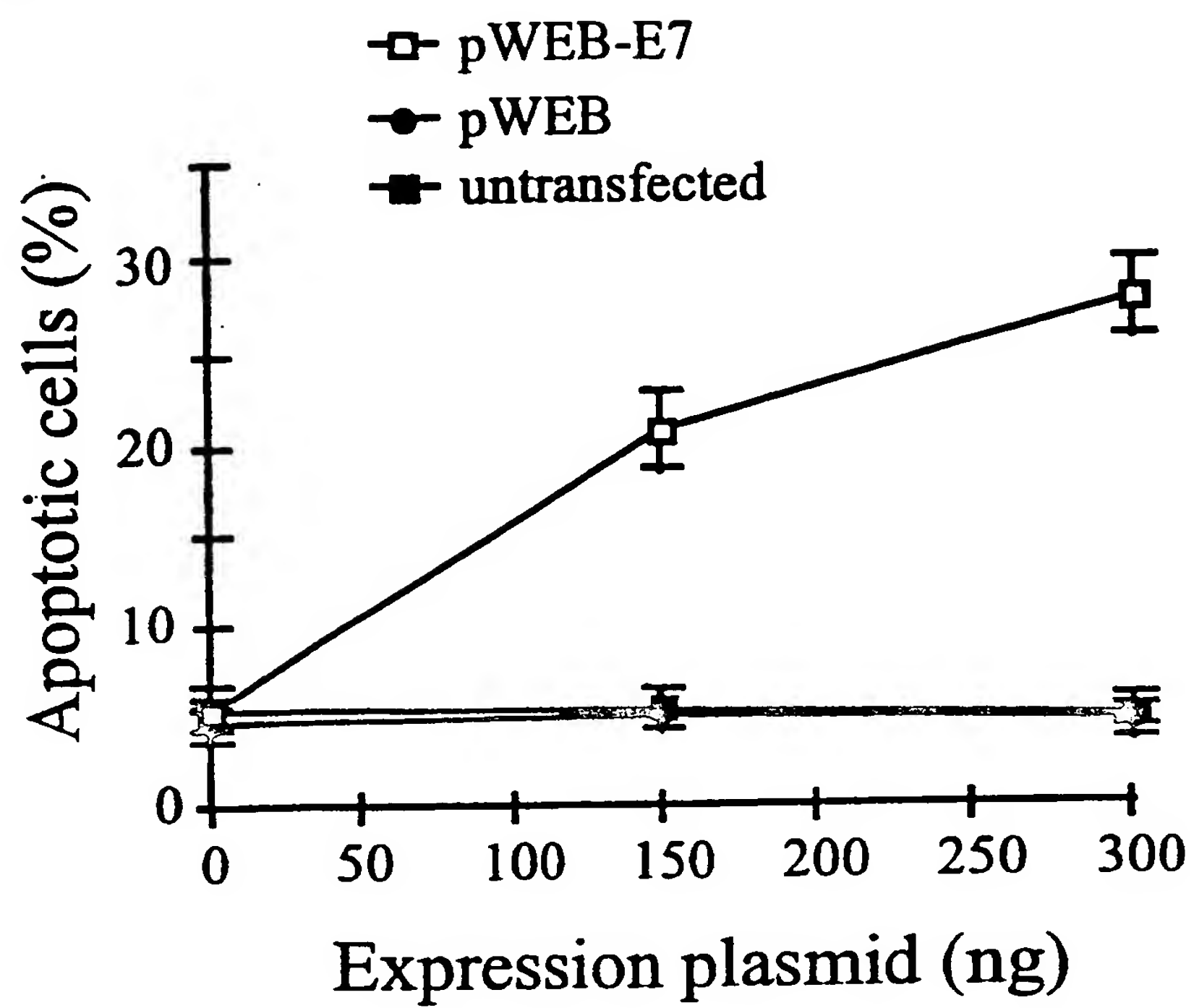


Fig. 3B

Fig. 4

a

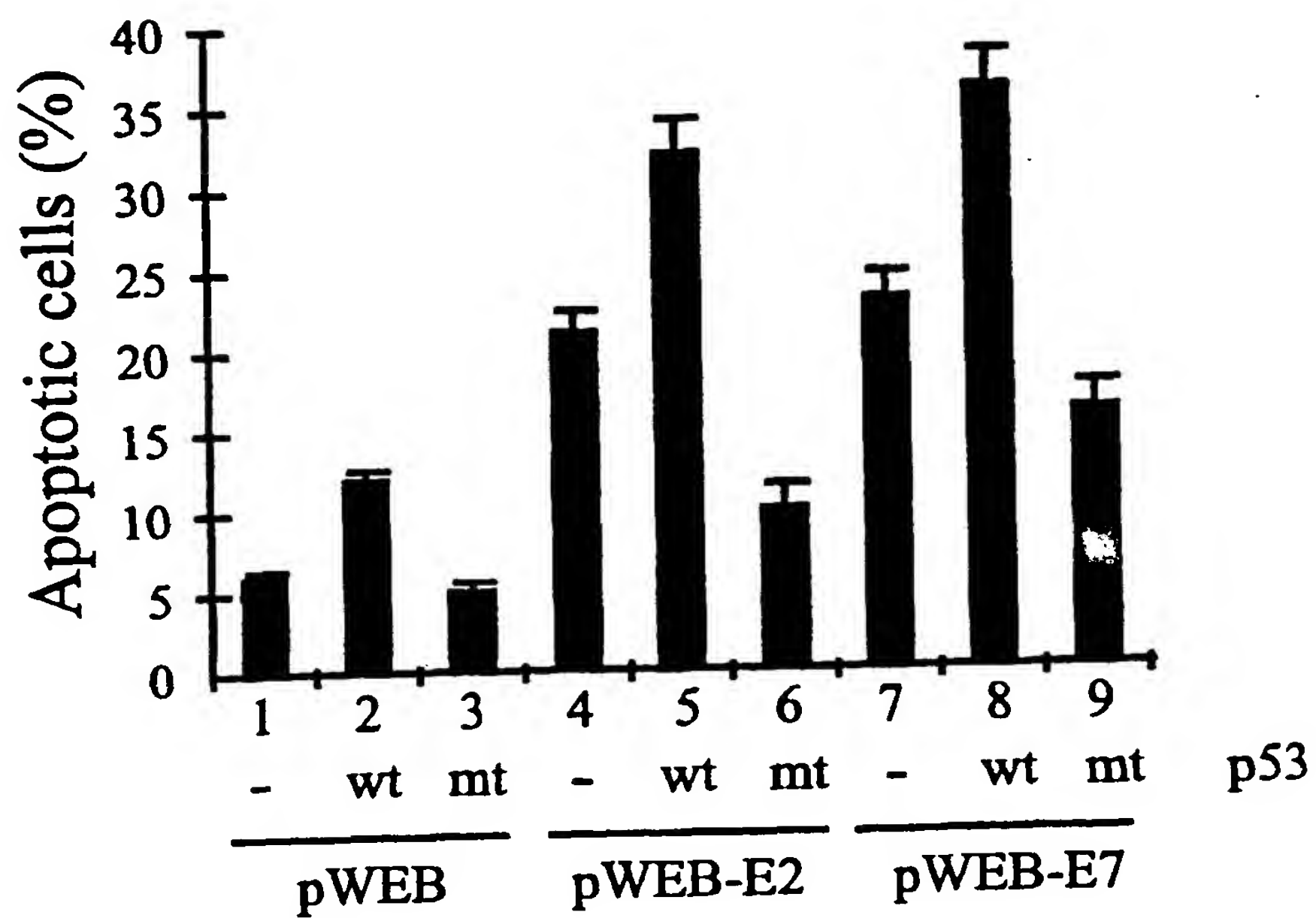


Fig. 4B

b

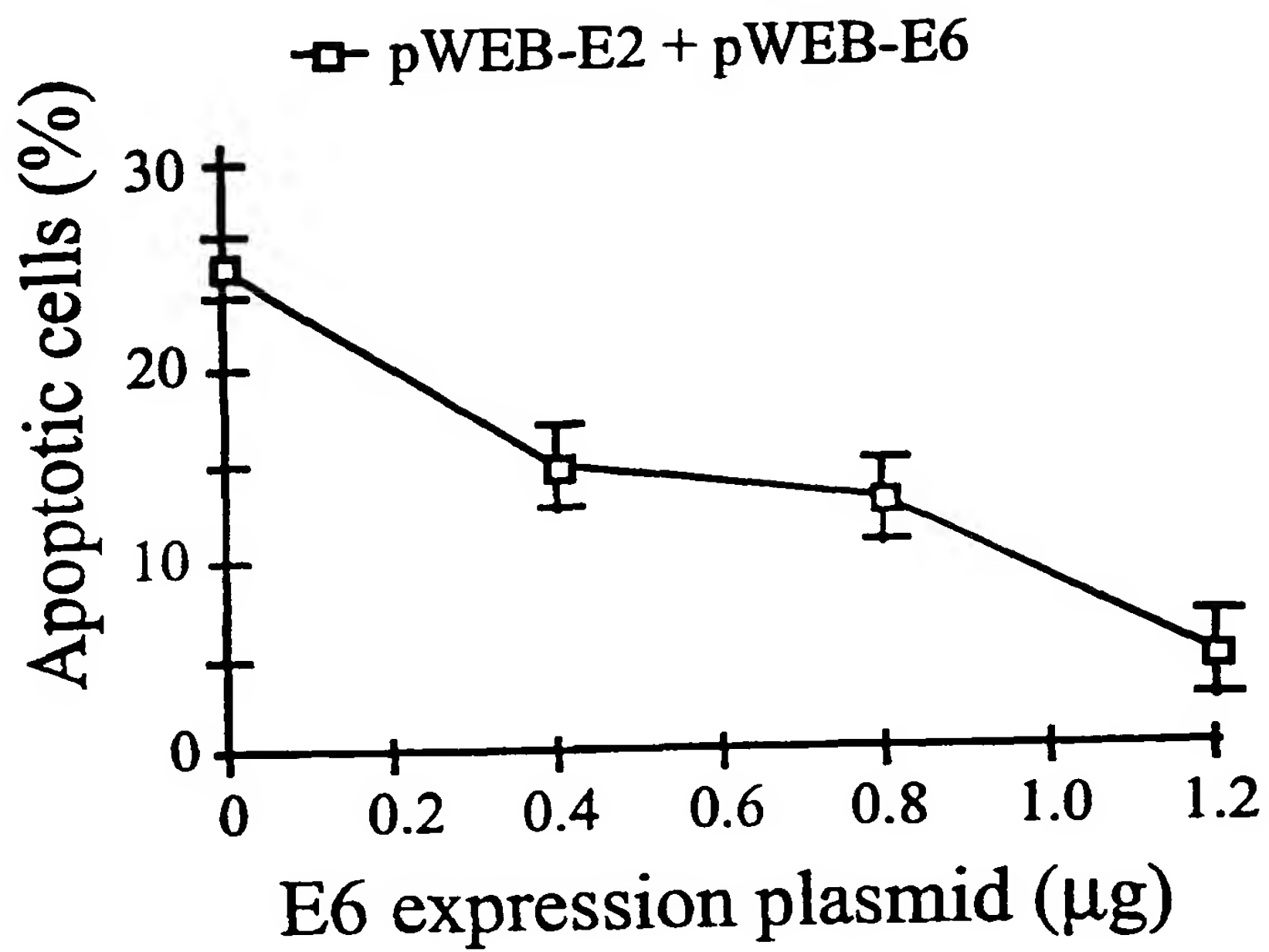
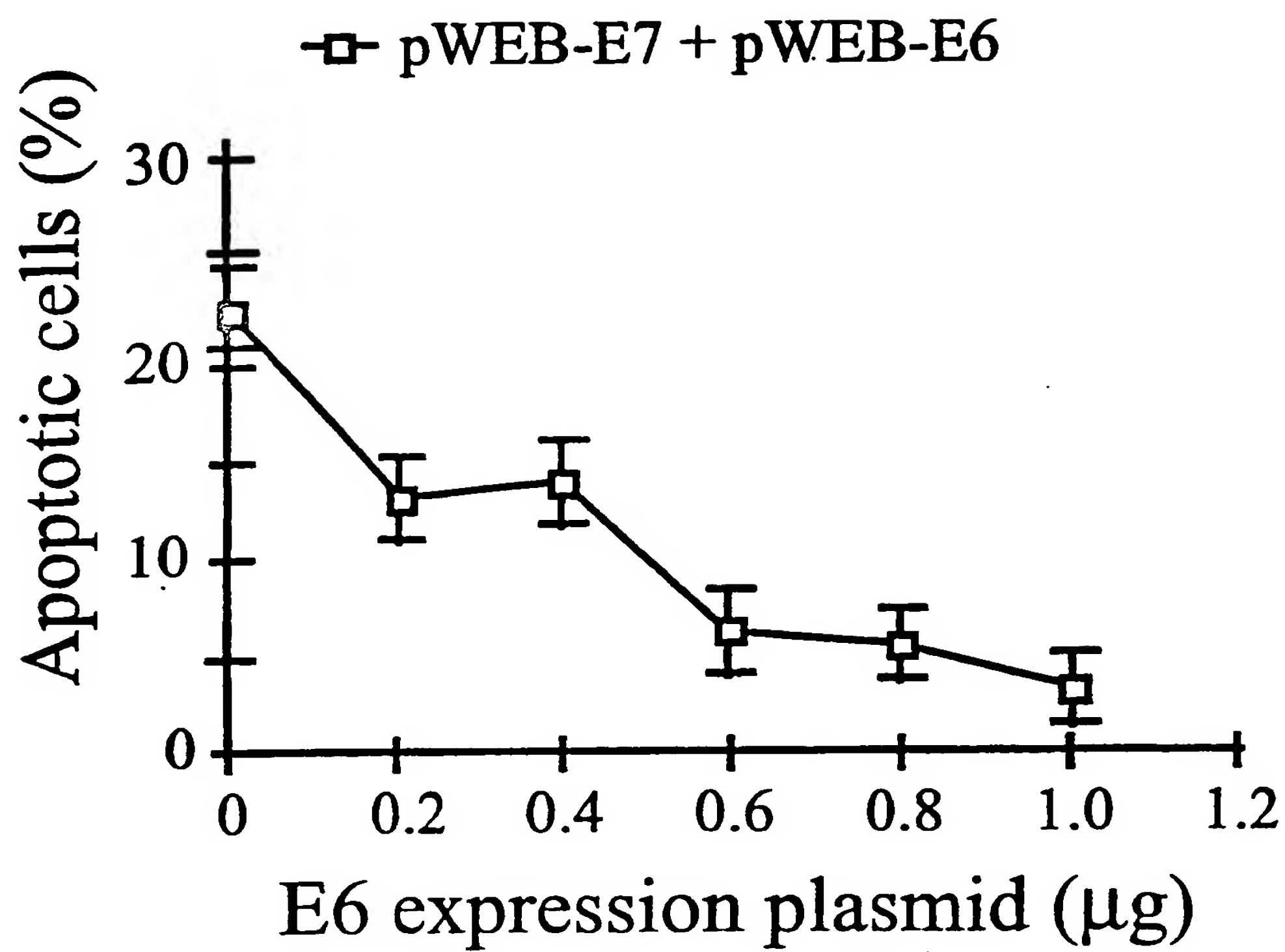


Fig 4C

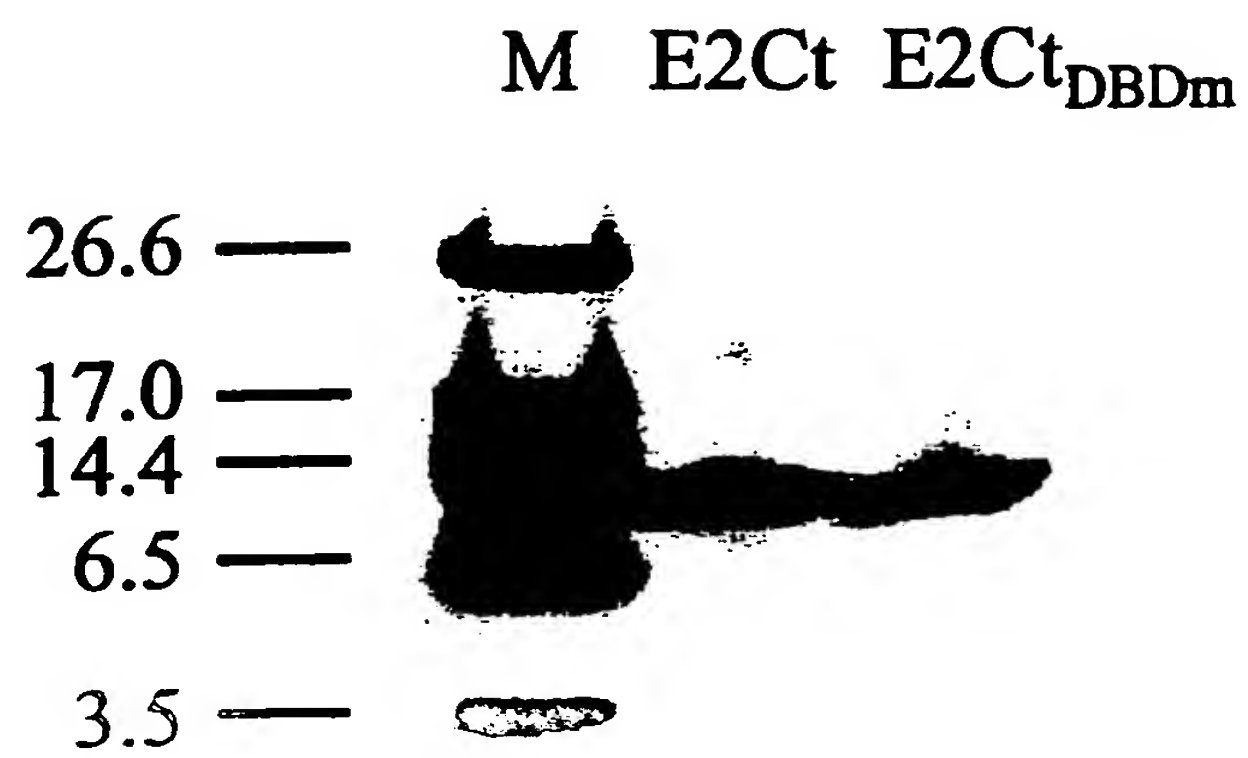
C



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Fig 5A

a



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Fig 5B

b

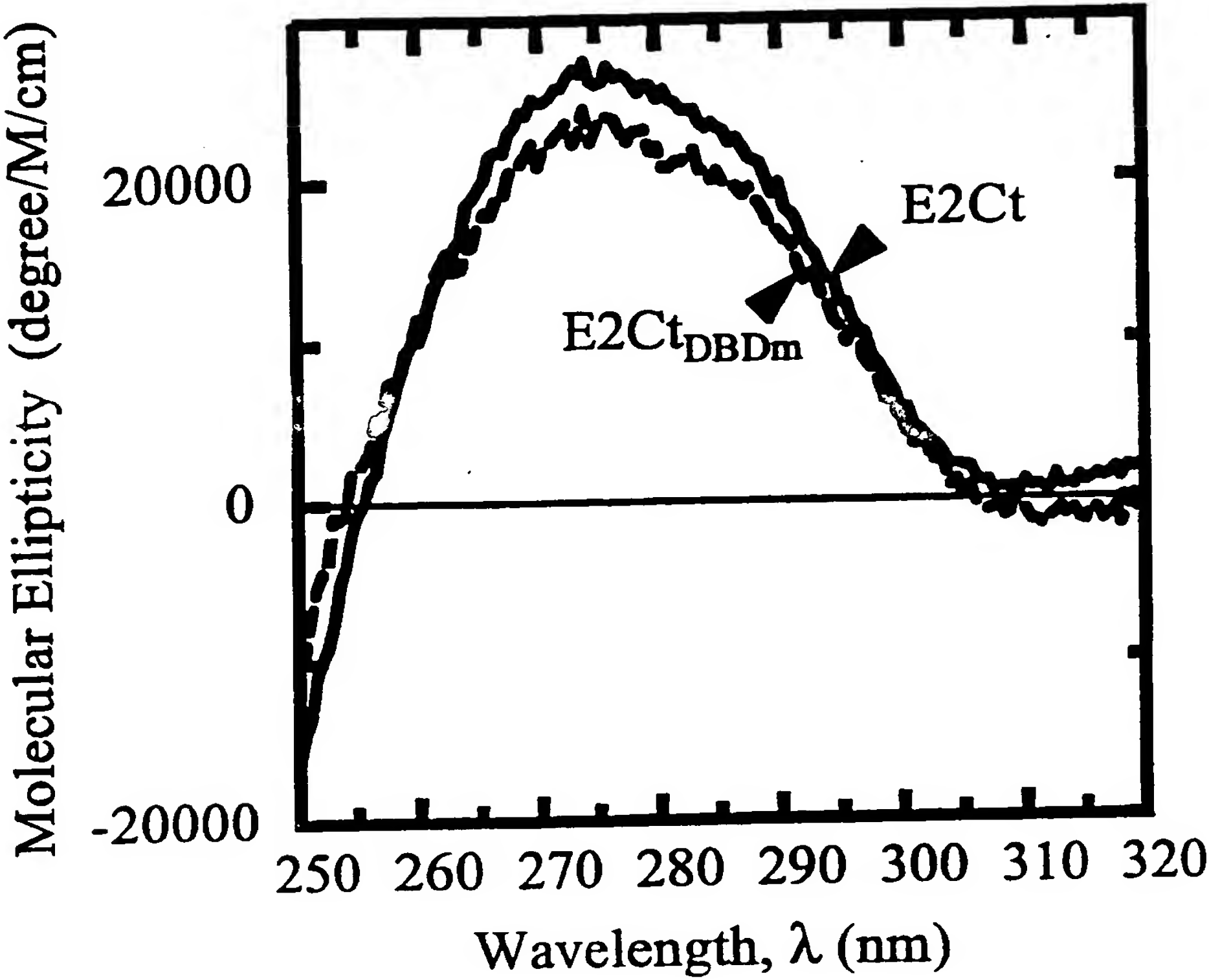


Fig 5C

C

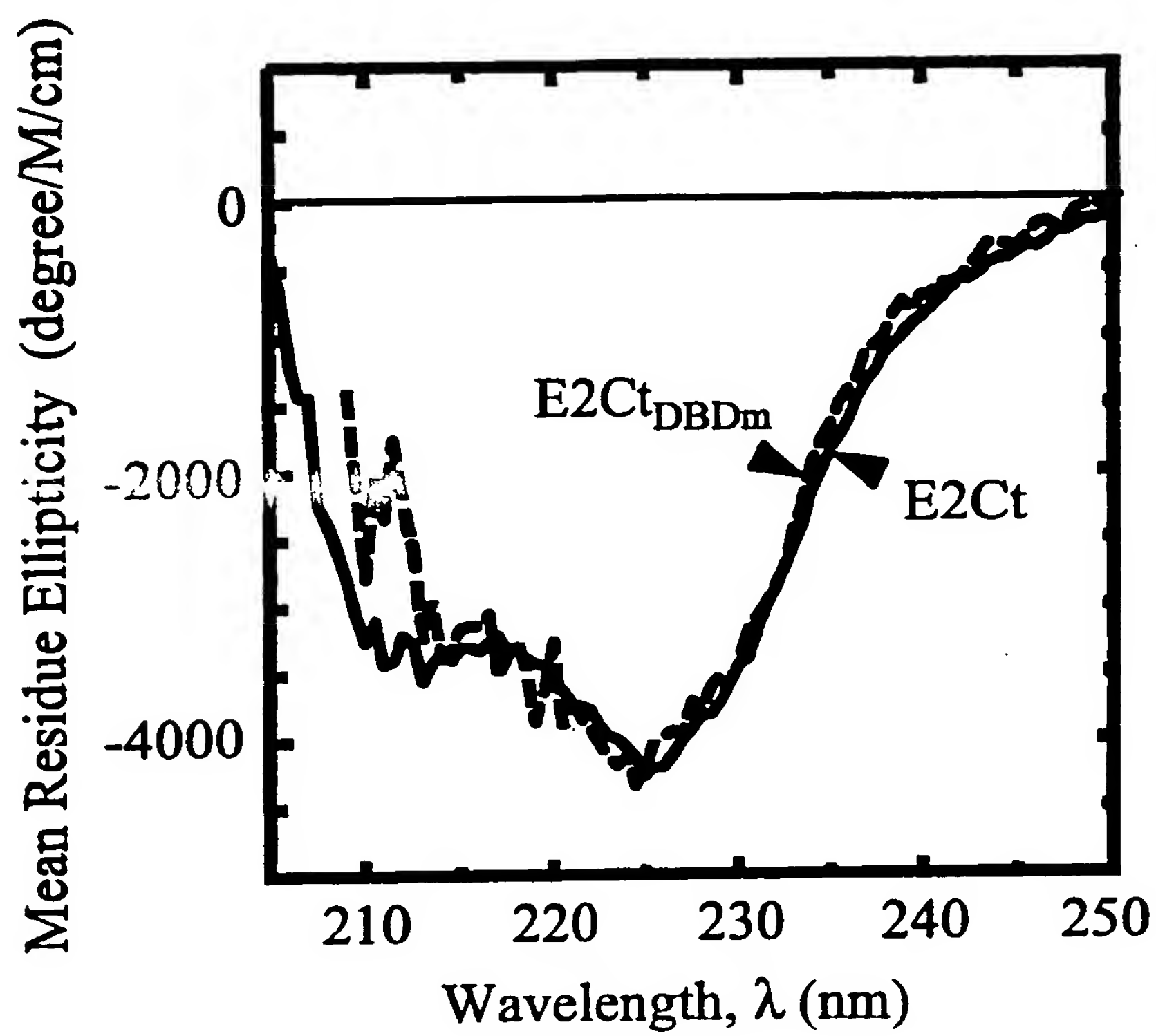
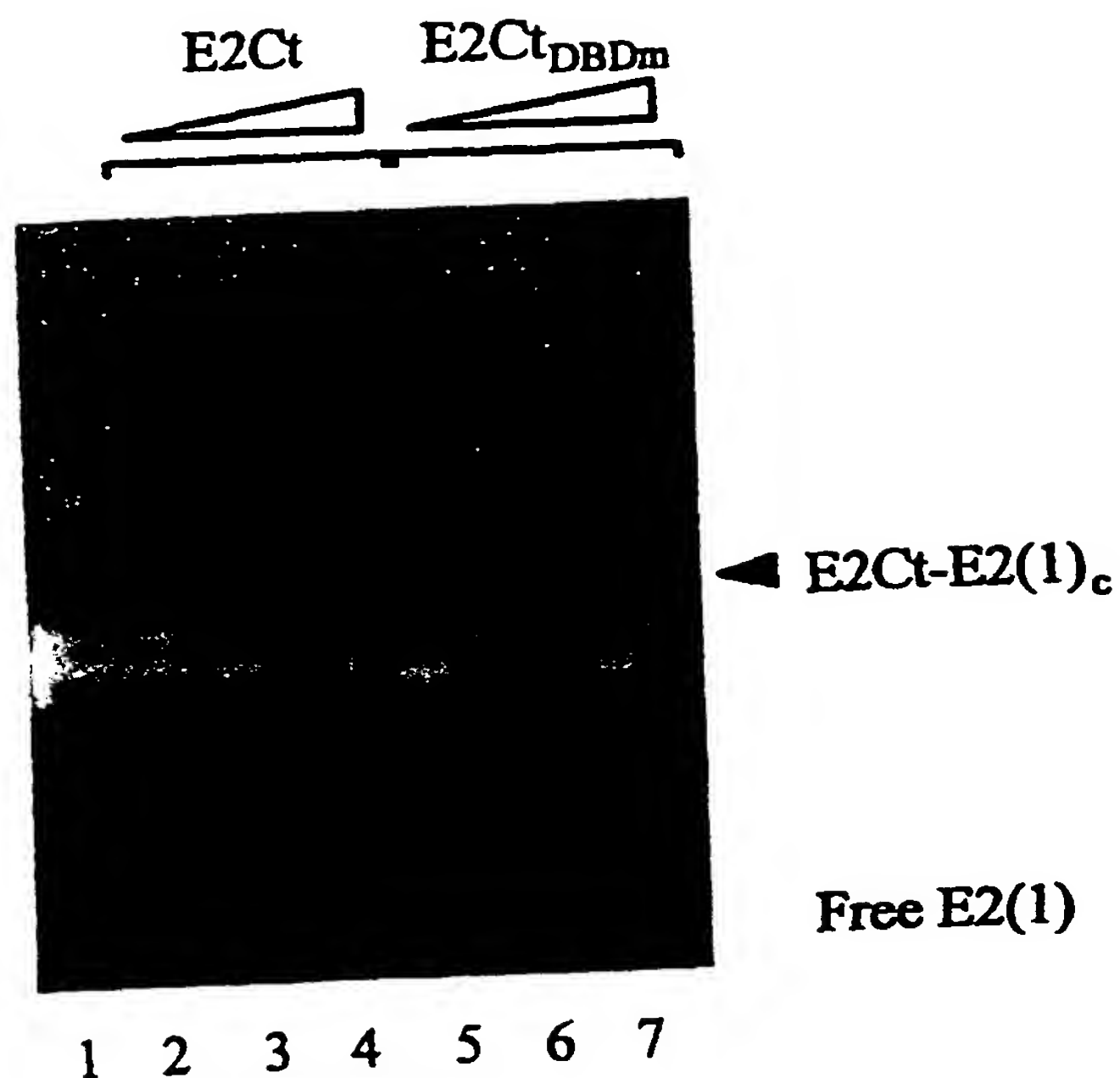


Fig 5D

d



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Fig. 6

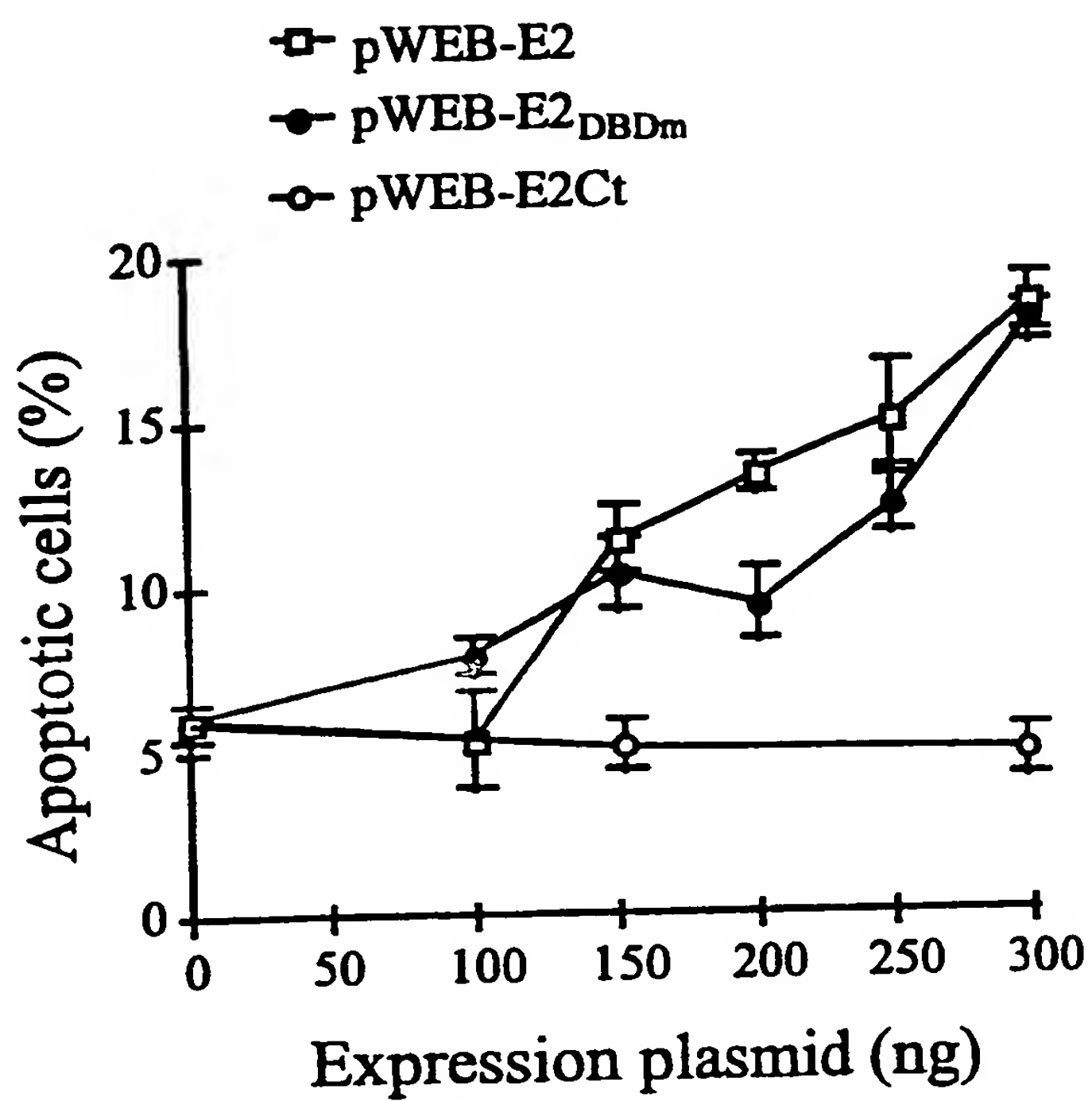
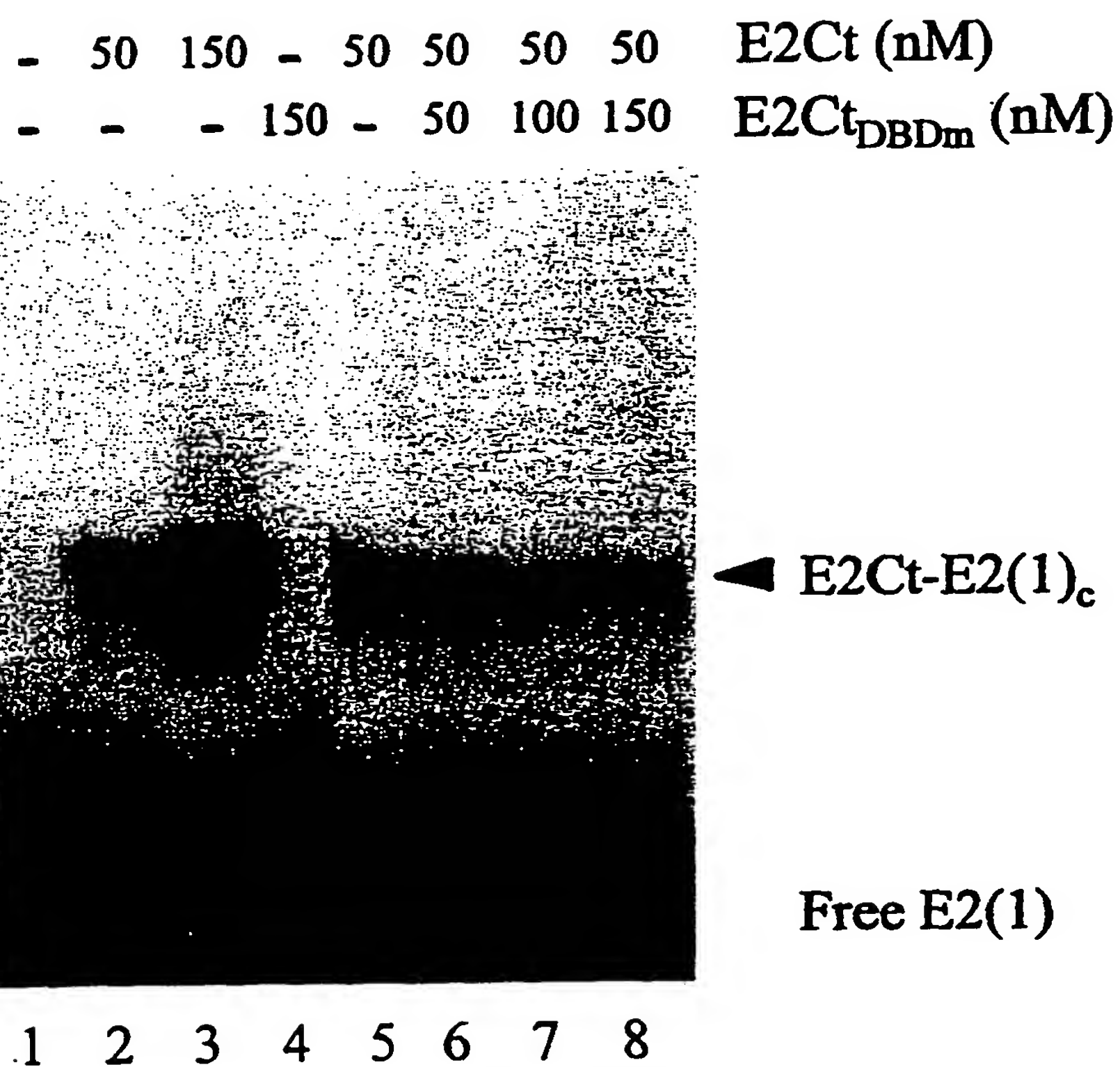


Fig. 7A

a



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Fig. 7B

b

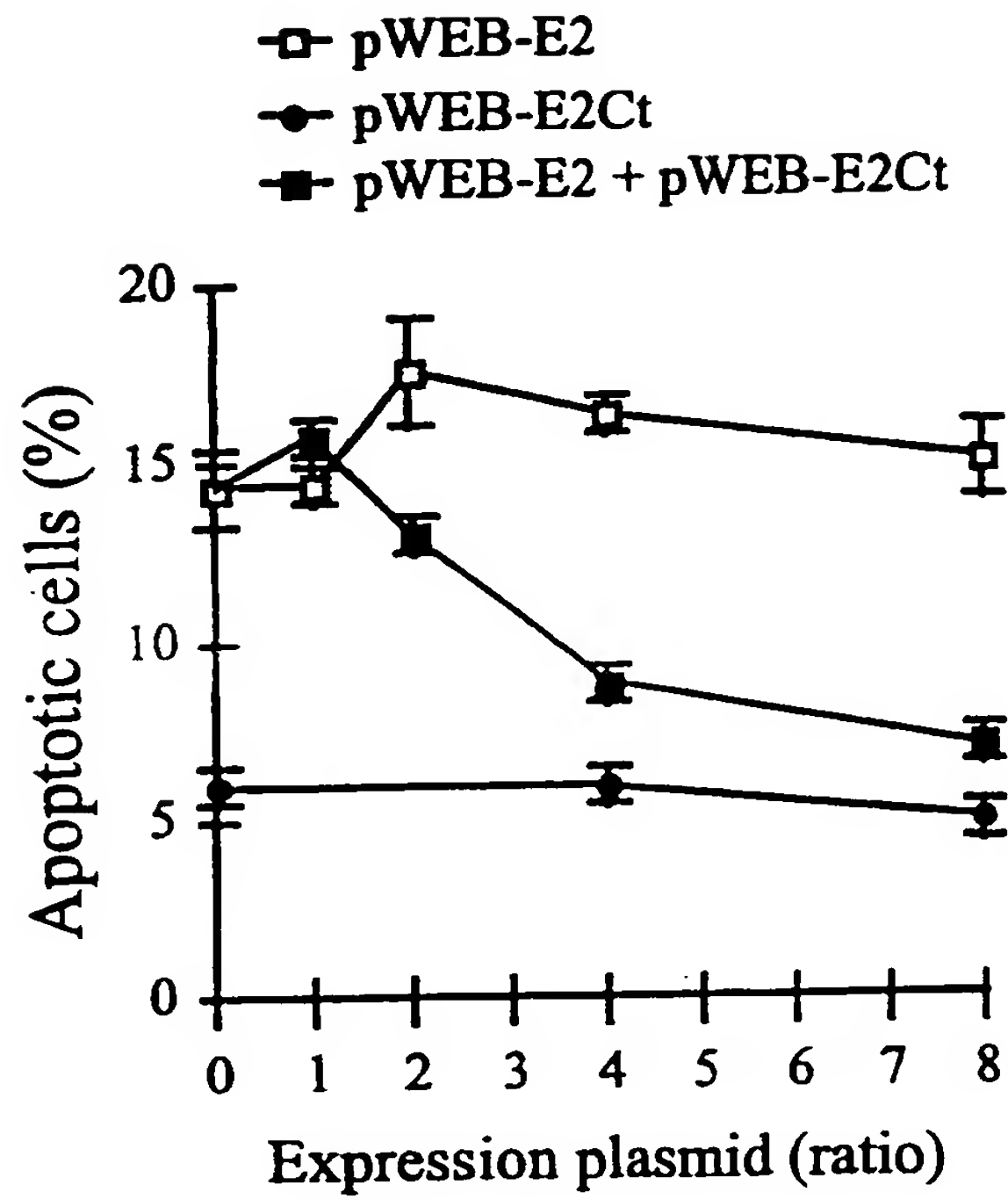
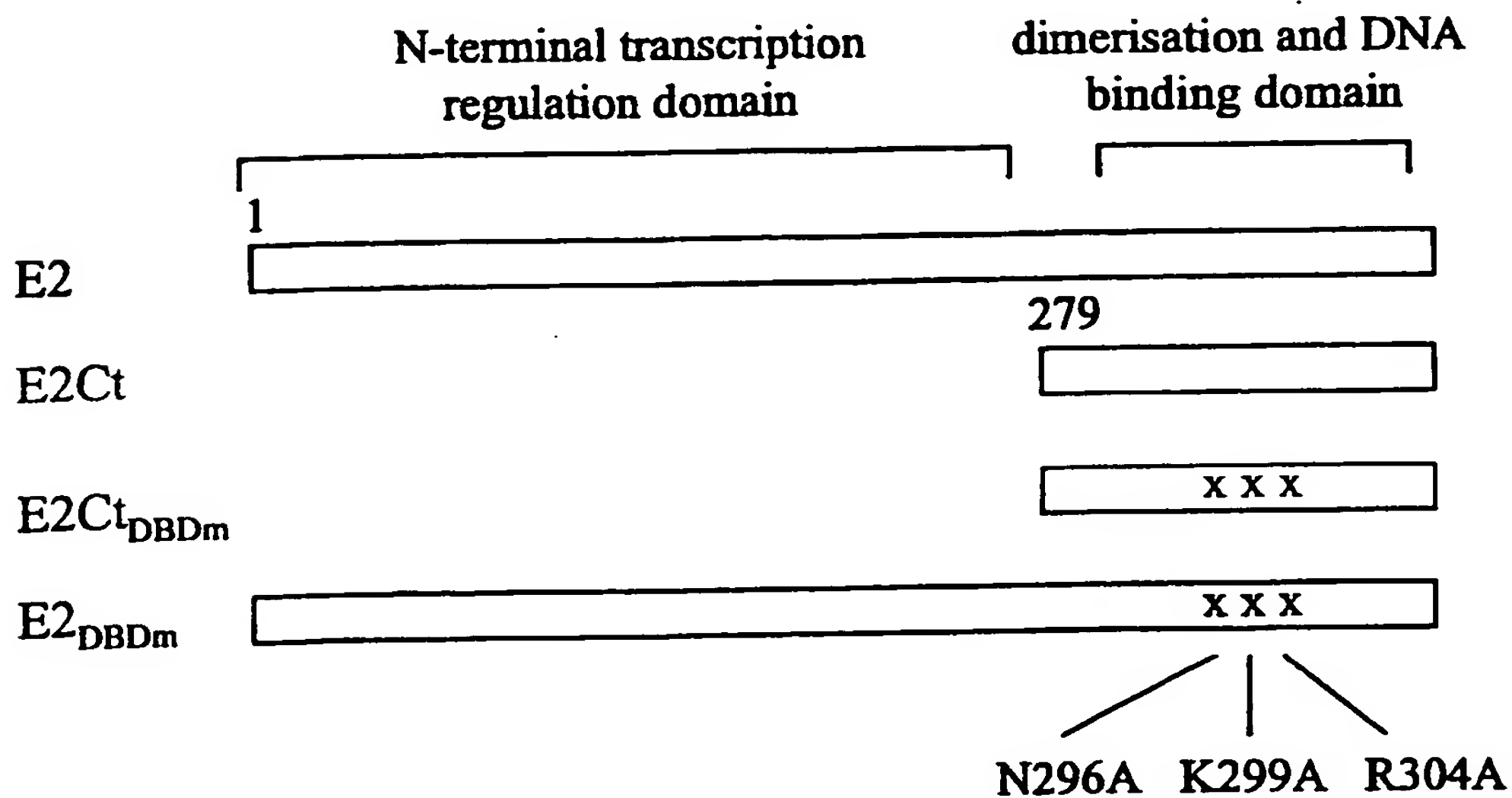


Fig. 8

The E2 proteins used in this work



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Fig. 9

HPV 16 E2

ATGGAGACTCTTTGCCAACGTTTAAATGTGTGTCAGGACAAAATACTAACACATTATGAA
2755 -----+-----+-----+-----+-----+-----+-----+-----
M E T L C Q R L N V C Q D K I L T H Y E

AATGATAGTACAGACCTACGTGACCATATAGACTATTGGAAACACATGCGCCTAGAATGT
2815 -----+-----+-----+-----+-----+-----+-----+-----
N D S T D L R D H I D Y W K H M R L E C

GCTATTTATTACAAGGCCAGAGAAATGGGATTTAAACATATTAACCACCAAGTGGTGCCA

2875 -----+-----+-----+-----+-----+-----+-----+-----
A I Y Y K A R E M G F K H I N H Q V V P

ACACTGGCTGTATCAAAGAATAAAGCATTACAAGCAATTGAACTGCAACTAACGTTAGAA
2935 -----+-----+-----+-----+-----+-----+-----+-----
T L A V S K N K A L Q A I E L Q L T L E

ACAATATATAACTCACAATATAGTAATGAAAAGTGGACATTACAAGACGTTAGCCTTGAA
2995 -----+-----+-----+-----+-----+-----+-----+-----
T I Y N S Q Y S N E K W T L Q D V S L E

GTGTATTTAACTGCACCAACAGGATGTATAAAAAACATGGATATACAGTGGGAAGTGCAG
3055 -----+-----+-----+-----+-----+-----+-----+-----
V Y L T A P T G C I K K H G Y T V E V Q

TTTGATGGAGACATATGCAATACAATGCATTATACAAACTGGACACATATATATTTGT
3115 -----+-----+-----+-----+-----+-----+-----+-----
F D G D I C N T M H Y T N W T H I Y I C

GAAGAAGCATCAGTAACTGTGGTAGAGGGTCAAGTTGACTATTATGGTTTATATTATGTT
3175 -----+-----+-----+-----+-----+-----+-----+-----
E E A S V T V V E G Q V D Y Y G L Y Y V

CATGAAGGAATACGAACATATTTTGTGCAGTTTAAAGATGATGCAGAAAAATATAGTAAA
3235 -----+-----+-----+-----+-----+-----+-----+-----
H E G I R T Y F V Q F K D D A E K Y S K

AATAAAGTATGGGAAGTTCATGCGGGTGGTCAGGTAATATTATGTCCTACATCTGTGTTT
3295 -----+-----+-----+-----+-----+-----+-----+-----
N K V W E V H A G G Q V I L C P T S V F

AGCAGCAACGAAGTATCCTCTCCTGAAATTATTAGGCAGCACTTGGCCAACCACCCCGCC
3355 -----+-----+-----+-----+-----+-----+-----+-----
S S N E V S S P E I I R Q H L A N H P A

GCGACCCATACCAAAGCCGTCGCCTTGGGCACCGAAGAAACACAGACGACTATCCAGCGA
3415 -----+-----+-----+-----+-----+-----+-----+-----

204400-065400T

A T H T K A V A L G T E E T Q T T I Q R

3475 CCAAGATCAGAGCCAGACACCGGAAACCCCTGCCACACCACTAAGTTGTTGCACAGAGAC
-----+-----+-----+-----+-----+-----+-----+-----
P R S E P D T G N P C H T T K L L H R D

3535 TCAGTGGACAGTGCTCCAATCCTCACTGCATTTAACAGCTCACACAAAGGACGGATTAAAC
-----+-----+-----+-----+-----+-----+-----+-----
S V D S A P I L T A F N S S H K G R I N

3595 TGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTAATACTTTAAAATGT
-----+-----+-----+-----+-----+-----+-----+-----
C N S N T T P I V H L K G D A N T L K C

3655 TTAAGATATAGATTTAAAAAGCATTGTACATTGTATACTGCAGTGTTCGTCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----+-----
L R Y R F K K H C T L Y T A V S S T W H

3715 TGGACAGGACATAATGTAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

3775 TGGCAACGTGACCAATTTTTGTCTCAAGTTAAAATACCAAAAACCTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

3835 GGATTTATGTCTATATGA 3852
-----+-----+-----
G F M S I * -

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Fig 10

HPV 16 E2DED_m

ATGGAGACTCTTTGCCAACGTTTAAATGTGTGTCAGGACAAAATACTAACACATTATGAA
2755 -----+-----+-----+-----+-----+-----+-----
M E T L C Q R L N V C Q D K I L T H Y E

AATGATAGTACAGACCTACGTGACCATATAGACTATTGGAAACACATGCGCCTAGAATGT
2815 -----+-----+-----+-----+-----+-----+-----
N D S T D L R D H I D Y W K H M R L E C

GCTATTTATTACAAGGCCAGAGAAATGGGATTTAAACATATTAACCACCAAGTGGTGCCA
2875 -----+-----+-----+-----+-----+-----+-----
A I Y Y K A R E M G F K H I N H Q V V P

ACACTGGCTGTATCAAAGAATAAAGCATTACAAGCAATTGAACTGCAACTAACGTTAGAA
2935 -----+-----+-----+-----+-----+-----+-----
T L A V S K N K A L Q A I E L Q L T L E

ACAATATATAACTCACAATATAGTAATGAAAAGTGGACATTACAAGACGTTAGCCTTGAA
2995 -----+-----+-----+-----+-----+-----+-----
T I Y N S Q Y S N E K W T L Q D V S L E

GTGTATTTAACTGCACCAACAGGATGTATAAAAAACATGGATATACAGTGAAGTGCAG
3055 -----+-----+-----+-----+-----+-----+-----
V Y L T A P T G C I K K H G Y T V E V Q

TTTGATGGAGACATATGCAATACAATGCATTATACAACTGGACACATATATATTTGT
3115 -----+-----+-----+-----+-----+-----+-----
F D G D I C N T M H Y T N W T H I Y I C

GAAGAAGCATCAGTAACTGTGGTAGAGGGTCAAGTTGACTATTATGGTTTATATTATGTT
3175 -----+-----+-----+-----+-----+-----+-----
E E A S V T V V E G Q V D Y Y G L Y Y V

CATGAAGGAATACGAACATATTTTGTGCAGTTTAAAGATGATGCAGAAAAATATAGTAAA
3235 -----+-----+-----+-----+-----+-----+-----
H E G I R T Y F V Q F K D D A E K Y S K

AATAAGTATGGGAAGTTCATGCGGGTGGTCAGGTAATATTATGTCCTACATCTGTGTTT
3295 -----+-----+-----+-----+-----+-----+-----
N K V W E V H A G G Q V I L C P T S V F

AGCAGCAACGAAGTATCCTCTCCTGAAATTATTAGGCAGCACTTGGCCAACCACCCCGCC
3355 -----+-----+-----+-----+-----+-----+-----
S S N E V S S P E I I R Q H L A N H P A

GCGACCCATACCAAAGCCGTCGCCTTGGGCACCGAAGAAACACAGACGACTATCCAGCGA
3415 -----+-----+-----+-----+-----+-----+-----
A T H T K A V A L G T E E T Q T T I Q R

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3475 CCAAGATCAGAGCCAGACACCGGAAACCCCTGCCACACCACTAAGTTGTTGCACAGAGAC
-----+-----+-----+-----+-----+-----+-----+-----
P R S E P D T G N P C H T T K L L H R D

3535 TCAGTGGACAGTGCTCCAATCCTCACTGCATTTAACAGCTCACACAAAGGACGGATTAAC
-----+-----+-----+-----+-----+-----+-----+-----
S V D S A P I L T A F N S S H K G R I N

3595 TGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTgctACTTTAgcaTGT
-----+-----+-----+-----+-----+-----+-----+-----
C N S N T T P I V H L K G D A A T L A C

3655 TTAAGATATgcaTTTAAAAGCATTGTACATTGTATACTGCAGTGTGCTCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----+-----
L R Y A F K K H C T L Y T A V S S T W H

3715 TGGACAGGACATAATGTAAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

3775 TGGCAACGTGACCAATTTTGTCTCAAGTTAAAATACCAAAAACCTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

3835 GGATTTATGTCTATATGA
-----+-----+----- 3852
G F M S I * -

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Fig 11

E2Ct

ATGAACTGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTAATACTTTAAAATGT
-----+-----+-----+-----+-----+-----+-----
M N C N S N T T P I V H L K G D A N T L K C

TTAAGATATAGATTTAAAAAGCATTGTACATTGTATACTGCAGTGTCGTCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----
L R Y R F K K H C T L Y T A V S S T W H

TGGACAGGACATAATGTAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

TGGCAACGTGACCAATTTTGTCTCAAGTTAAAATACCAAAAACCTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

GGATTTATGTCTATATGA
-----+-----+----- 3852
G F M S I * -

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Fig 12

E2CtDBDm

ATGAACTGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTgctACTTTAgcaTGT
-----+-----+-----+-----+-----+-----+-----+-----+-----
M N C N S N T T P I V H L K G D A A T L A C

TTAAGATATgcaTTTAAAAAGCATTGTACATTGTATACTGCAGTGTCTGCTCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----+-----+-----
L R Y A F K K H C T L Y T A V S S T W H

TGGACAGGACATAATGTAAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

TGGCAACGTGACCAATTTTTGTCTCAAGTTAAAATACCAAAAACCTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

GGATTTATGTCTATATGA
-----+-----+----- 3852
G F M S I * -

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Fig 13

